

STIC-Biotech/ChemLib

175 266 me

From: Haddad, Maher
Sent: Thursday, December 29, 2005 7:31 AM
To: STIC-Biotech/ChemLib
Subject: 09/937,076

RECEIVED
DEC 29 2005
STIC-BIOTECH LIB
(STIC)

Maher Haddad, 1644
REM 3D79/3C70
(571) 272-0845

Please search both commercial and interference data bases for

SEQ ID NO: 3 (close, i.e., 100% over the exact length).

Thanks

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIF: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 09:03:59 ; Search time 376 Seconds
(without alignments)
9.348 Million cell updates/sec

Title: US-09-937-076A-3
Perfect score: 8
Sequence: 1 QPPRAAIY 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 8

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Listing first 1000 summaries

- Database : A_Geneseq_21.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004s.*
 - 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	100.0	8	3 AAB19055	Aab19055 Amino aci

ALIGNMENTS

RESULT 1
-AAB19055
ID AAB19055 standard; peptide; 8 AA.
XX
AC AAB19055;
XX
-FT 08-FEB-2001 (first entry)
XX
DE Amino acid sequence of a betal-integrin inhibitor.
XX
KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;
KW central nervous system ischemic injury; myocardial infarction;
KW betal-integrin; angioplasty; surgical incision; injury-related trauma;
KW transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
OS Synthetic.
XX
PN WO200056350-A2.

XX 28-SEP-2000.
XX PD
XX PF 22-MAR-2000; 2000WO-US007680.
XX XX
XX PR 22-MAR-1999; 99US-0125634P.
XX PR 24-NOV-1999; 99US-0167538P.
XX XX
XX PA (MINU) UNIV MINNESOTA.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PA (SENT-) SENTRON MEDICAL INC.
XX XX
XX PI McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
XX PI Furcht LT;
XX XX
XX DR WPI; 2000-658062/63.
XX XX
XX PT Inhibition of inflammatory leukocyte mediated destruction of tissue in a
XX PT patient, comprises administering a peptide inhibitor of betal-integrin,
XX PT useful for treatment of e.g. cancer and osteoporosis.
XX XX
XX PS Claim 3; Page 38; 61pp; English.
XX XX
XX CC AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit
XX CC betal-integrin which is responsible for leukocyte mediated tissue
XX CC destruction. The peptides are useful for inhibiting inflammatory
XX CC leukocyte mediated destruction of tissue which occurs as a result of
XX CC central nervous system (CNS) ischemic injury, myocardial infarction,
XX CC angioplasty, surgical incisions, injury-related trauma, and/or transplant
XX CC reperfusion, exposure to heat, cold, light, electricity and/or chemicals.
XX CC They are also useful for the treatment of stroke, a burn type injury,
XX CC cancer, and osteoporosis
XX XX
XX SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QPPRAAIY 8
Db 1 QPPRAAIY 8

Search completed: January 5, 2006, 09:11:30
Job time : 380 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 09:12:30 ; Search time 73 Seconds
(without alignments)
10.544 Million cell updates/sec

Title: US-09-937-076A-3
Perfect score: 8
Sequence: 1 QPPRAAY 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 8

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Listing first 1000 summaries

Database : PIR_80.*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

No matches found

Search completed: January 5, 2006, 09:22:07
Job time : 75 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 09:05:08 ; Search time 515 Seconds
(without alignments)
10.960 Million cell updates/sec

Title: US-09-937-076A-3
Perfect score: 8
Sequence: 1 QPPRAAY 8

Scoring table: OLIGO /
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size: 8

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Listing first 1000 summaries

Database: UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred.No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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.No matches found

Search completed: January 5, 2006, 09:20:33
Job time : 522 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 09:47:19 ; Search time 106 Seconds
(without alignments)
6.240 Million cell updates/sec

Title: US-09-937-076A-3
Perfect score: 8
Sequence: 1 QPPRAAIY 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 8

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

No matches found

Search completed: January 5, 2006, 09:56:44
Job time : 108 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 09:47:19 ; Search time 409 Seconds
(without alignments)
8.173 Million cell updates/sec

Title: US-09-937-076A-3
Perfect score: 8
Sequence: 1 QPPRAAIY 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 8

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Listing first 1000 summaries

Database : Published Applications AA Main.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
No.						

No matches found

Search completed: January 5, 2006, 09:54:41
Job time : 412 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 09:56:37 ; Search time 14 Seconds
(without alignments)
4.850 Million cell updates/sec

Title: US-09-937-076A-3

Perfect score: 8

Sequence: 1 QPPRAIY 8

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size: 8

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Listing first 1000 summaries

Database : Published Applications AA New.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

No matches found					

Search Completed: January 5, 2006, 09:57:07
Job time : 15 secs